SEQUENCE LISTING

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<120> DNA Encoding a Novel PROST 03

<130> 51831AUSM1

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<150> 60/200,065
<151> 2000-04-27

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<170> PatentIn Ver. 2.0

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gctggaccgg caccaaaggg ctggcagaaa tgggcgcctg gctgattcct aggcagttgg 180

cggcagcaag gaggagaggc cgcagcttct ggagcagagc cgagacgaag cagttctgga 240

gtgcctgaac ggccccctga gccctacccg cctggcccac t atg gtc cag agg ctg 296
                                              Met Val Gln Arg Leu
                                                1   5

tgg gtg agc cgc ctg ctg cgg cac cgg aaa gcc cag ctc ttg ctg gtc 344
Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala Gln Leu Leu Leu Val
               10   15   20

aac ctg cta acc ttt ggc ctg gag gtg tgt ttg gcc gca ggc atc acc 392
Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu Ala Ala Gly Ile Thr
            25   30   35

1

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tat gtg ccg cct ctg ctg ctg gaa gtg ggg gta gag gag aag ttc atg    440
Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val Glu Glu Lys Phe Met
        40              45              50

acc atg gtg ctg ggc att ggt cca gtg ctg ggc ctg gtc tgt gtc ccg    488
Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro
        55              60              65

ctc cta ggc tca gcc agt gac cac tgg cgt gga cgc tat ggc cgc cgc    536
Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg
70              75              80              85

cgg ccc ttc atc tgg gca ctg tcc ttg ggc atc ctg ctg agc ctc ttt    584
Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe
                90              95              100

ctc atc cca agg gcc ggc tgg cta gca ggg ctg ctg tgc ccg gat ccc    632
Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro
                105             110             115

agg ccc ctg gag ctg gca ctg ctc atc ctg ggc gtg ggg ctg ctg gac    680
Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp
        120             125             130

ttc tgt ggc cag gtg tgc ttc act cca ctg gag gcc ctg ctc tct gac    728
Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp
        135             140             145

ctc ttc cgg gac ccg gac cac tgt cgc cag gcc tac tct gtc tat gcc    776
Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala
150             155             160             165

ttc atg atc agt ctt ggg ggc tgc ctg ggc tac ctc ctg cct gcc att    824
Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile
                170             175             180

gac tgg gac acc agt gcc ctg gcc ccc tac ctg ggc acc cag gag gag    872
Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu
                185             190             195

tgc ctc ttt ggc ctg ctc acc ctc atc ttc ctc acc tgc gta gca gcc    920
Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala
        200             205             210

aca ctg ctg gtg gct gag gag gca gcg ctg ggc ccc acc gag cca gca    968
Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala
        215             220             225

gaa ggg ctg tcg gcc ccc tcc ttg tcg ccc cac tgc tgt cca tgc cgg    1016
Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg
230             235             240             245

gcc cgc ttg gct ttc cgg aac ctg ggc gcc ctg ctt ccc cgg ctg cac    1064
Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His
                250             255             260
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2

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cag ctg tgc tgc cgc atg ccc cgc acc ctg cgc cgg ctc ttc gtg gct    1112
Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala
        265                 270                 275

gag ctg tgc agc tgg atg gca ctc atg acc ttc acg ctg ttt tac acg    1160
Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr
        280                 285                 290

gat ttc gtg ggc gag ggg ctg tac cag ggc gtg ccc aga gct gag ccg    1208
Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro
        295                 300                 305

ggc acc gag gcc cgg aga cac tat gat gaa ggc gtt cgg atg ggc agc    1256
Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser
310                 315                 320                 325

ctg ggg ctg ttc ctg cag tgc gcc atc tcc ctg gtc ttc tct ctg gtc    1304
Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val
                330                 335                 340

atg gac cgg ctg gtg cag cga ttc ggc act cga gca gtc tat ttg gcc    1352
Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala
                345                 350                 355

agt gtg gca gct ttc cct gtg gct gcc ggt gcc aca tgc ctg tcc cac    1400
Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His
        360                 365                 370

agt gtg gcc gtg gtg aca gct tca gcc gcc ctc acc ggg ttc acc ttc    1448
Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe
        375                 380                 385

tca gcc ctg cag atc ctg ccc tac aca ctg gcc tcc ctc tac cac cgg    1496
Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg
390                 395                 400                 405

gag aag cag gtg ttc ctg ccc aaa tac cga ggg gac act gga ggt gct    1544
Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala
                410                 415                 420

agc agt gag gac agc ctg atg acc agc ttc ctg cca ggc cct aag cct    1592
Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro
                425                 430                 435

gga gct ccc ttc cct aat gga cac gtg ggt gct gga ggc agt ggc ctg    1640
Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu
            440                 445                 450

ctc cca cct cca ccc gcg ctc tgc ggg gcc tct gcc tgt gat gtc tcc    1688
Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser
        455                 460                 465

gta cgt gtg gtg gtg ggt gag ccc acc gag gcc agg gtg gtt ccg ggc    1736
Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly
470                 475                 480                 485
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3

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cgg ggc atc tgc ctg gac ctc gcc atc ctg gat agt gcc ttc ctg ctg    1784
Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu
              490                 495                 500

tcc cag gtg gcc cca tcc ctg ttt atg ggc tcc att gtc cag ctc agc    1832
Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser
              505                 510                 515

cag tct gtc act gcc tat atg gtg tct gcc gca ggc ctg ggt ctg gtc    1880
Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val
              520                 525                 530

gcc att tac ttt gct aca cag gta gta ttt gac aag agc gac ttg gcc    1928
Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala
              535                 540                 545

aaa tac tca gcg tag aaaacttcca gcacattggg gtggagggcc tgcctcactg    1983
Lys Tyr Ser Ala
550


ggtcccagct ccccgctcct gttagcccca tggggctgcc gggctggccg ccagtttctg 2043

ttgctgccaa agtaatgtgg ctctctgctg ccaccctgtg ctgctgaggt gcgtagctgc 2103

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aactttcccc tacccccaac tttccccacc agctccacaa ccctgtttgg agctactgca 3063

ggaccagaag cacaaagtgc ggtttcccaa gcctttgtcc atctcagccc ccagagtata 3123
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4

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tctgtgcttg gggaatctca cacagaaact caggagcacc ccctgcctga gctaagggag 3183

gtcttatctc tcaggggggg gtttaagtgc cgtttgcaat aatgtcgtct tatttatta 3243

gcggggtgaa tattttatac tgtaagtgag caatcagagt ataatgttta tggtgacaaa 3303

attaaaggct ttcttat                                                3320
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<212> PRT
<213> Homo sapiens

<400> 2

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Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
            20                  25                  30

Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
        35                  40                  45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
    50                  55                  60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
65                  70                  75                  80

Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
                85                  90                  95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
            100                 105                 110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
            115                 120                 125

Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
    130                 135                 140

Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
145                 150                 155                 160

Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
                165                 170                 175

Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
            180                 185                 190

Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
            195                 200                 205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
    210                 215                 220
```

5

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Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
225             230             235             240

Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
            245             250             255

Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
        260             265             270

Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
        275             280             285

Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
    290             295             300

Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
305             310             315             320

Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
            325             330             335

Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
        340             345             350

Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
        355             360             365

Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
370             375             380

Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
385             390             395             400

Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
            405             410             415

Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
            420             425             430

Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
        435             440             445

Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser
    450             455             460

Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
465             470             475             480

Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
            485             490             495

Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
        500             505             510

Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
        515             520             525
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6

Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
    530   535   540

Lys Ser Asp Leu Ala Lys Tyr Ser Ala
545   550

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<211> 22
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 3
ggtggcgacg actcctggag cc   22

<210> 4
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 4
gacaccagac caactggtaa tg   22

<210> 5
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 5
cacctccagt gtcccctcgg tatttgg   27

<210> 6
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<400> 6
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<210> 7
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 7
actgaattcg ccaccatggt ccagaggctg tgg   33

<210> 8
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 8
ccatccagct gcacagctca g   21

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 9
cctcccaggc tctgtctgat   20

<210> 10
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 10
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<210> 11
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<212> DNA
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<220>
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<400> 11
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<210> 12
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<220>
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<210> 13
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 13
tgagggcggc tgaagct                                                17


<210> 14
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: probe

<400> 14
caggcatgtg gcaccggca                                              19


<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 15
cagccagtct gtcactgcct at                                          22


<210> 16
<211> 27
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: primer

<400> 16
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<210> 17
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: probe

<400> 17
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<210> 18
<211> 14
<212> PRT
<213> Homo sapiens

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 1   5   10

<210> 19
<211> 18
<212> PRT
<213> Homo sapiens

<400> 19
Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala
 1   5   10   15

Glu Pro

<210> 20
<211> 16
<212> PRT
<213> Homo sapiens

<400> 20
Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met
 1   5   10   15

<210> 21
<211> 26
<212> PRT
<213> Homo sapiens

<400> 21
Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala
1   5   10   15

Ser Ser Glu Asp Ser Leu Met Thr Ser Phe
                20   25

<210> 22
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<212> PRT
<213> Homo sapiens

<400> 22
Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu
1   5   10

<210> 23
<211> 17
<212> PRT
<213> Homo sapiens

<400> 23
Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu
1   5   10   15

Glu

<210> 24
<211> 10
<212> PRT
<213> Homo sapiens

<400> 24
Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala
1   5   10

<210> 25
<211> 28
<212> PRT
<213> Homo sapiens

<400> 25
Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Gly
1   5   10   15

Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg
                20   25

<210> 26
<211> 16
<212> PRT
<213> Homo sapiens

<400> 26
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
1   5   10   15